
W P S R A L

(TM)

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MPSrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu Dec 23 10:13:23 1999; MasPar time 2.04 Seconds
83.062 Million cell updates/sec

Tabular output not generated.

Title: >US-09-177-843-2
Description: (1-6) from US09177843.ppe
Perfect Score: 41
Sequence: 1 GRGESP 6

Scoring table: PAM 150
Gap 15

Searched: 77977 seqs, 28268293 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot37
i:swissprot

Statistics: Mean 18.780; Variance 16.567; scale 1.134

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES						
Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	40	97.6	1256	1	FINC_CHICK FIBRONECTIN (FN) (FRAG	1.94e+00
2	40	97.6	1328	1	FINC_PLEWA FIBRONECTIN (FN) (FRAG	1.94e+00
3	40	97.6	2265	1	FINC_BOVIN FIBRONECTIN (FN)	1.94e+00
4	40	97.6	2386	1	FINC_HUMAN FIBRONECTIN PRECURSOR	1.94e+00
5	40	97.6	2477	1	FINC_MOUSE FIBRONECTIN PRECURSOR	1.94e+00
6	40	97.6	2477	1	FINC_RAT FIBRONECTIN PRECURSOR	1.94e+00
7	40	97.6	2481	1	FINC_XENLA FIBRONECTIN PRECURSOR	1.94e+00
8	39	95.1	425	1	YIK3_YEAST HYPOTHETICAL 48.3 KD P	3.67e+00
9	39	95.1	463	1	Y863_SYN3 HYPOTHETICAL 50.4 KD P	3.67e+00
10	38	92.7	336	1	FILA_MOUSE FILAGGRIN (FRAGMENT)	6.87e+00
11	38	92.7	370	1	HUPK_RHILV HYDROGENASE EXPRESSION	6.87e+00
12	38	92.7	492	1	CPS3_PIG CYTOCHROME P450 XXIA3	6.87e+00
13	38	92.7	492	1	CPS1_PIG CYTOCHROME P450 XXIA1	6.87e+00
14	38	92.7	495	1	CPBL_BOVIN CYTOCHROME P450 2E1 (E	6.87e+00
15	38	92.7	953	1	YNN7_YEAST HYPOTHETICAL 109.8 KD	6.87e+00
16	37	90.2	825	1	SE5_RAT 5E5 ANTIGEN	1.27e+01
17	37	90.2	1266	1	NGCA_CHICK NEURONAL-GLIAL CELL AD	1.27e+01
18	36	87.8	165	1	RS10_XENLA 40S RIBOSOMAL PROTEIN	2.31e+01
19	36	87.8	235	1	NHAB_RHOSO NITRILE HYDRATASE SUBU	2.31e+01
20	36	87.8	490	1	PCB8_HUMAN CYTOCHROME P450 2C8 (E	2.31e+01
21	36	87.8	583	1	PUP6_CRYNE PHOSPHORIBOSYLAMINOIM	2.31e+01
22	36	87.8	657	1	MY16_MOUSE MYELOID DIFFERENTIATIO	2.31e+01
23	36	87.8	715	1	Y07J_MYCTU HYPOTHETICAL 78.2 KDP	2.31e+01

ALIGNMENTS									
RESULT 1									
ID	FINC_CHICK	STANDARD;	PRT;	1256	AA.				
AC	P11722	Q90921;							
DT	01-OCT-1989	(REL. 12, CREATED)							
DT	01-NOV-1997	(REL. 35, LAST SEQUENCE UPDATE)							
DT	01-NOV-1997	(REL. 35, LAST ANNOTATION UPDATE)							
DE	FIBRONECTIN (FN) (FRAGMENTS).								
GN	FNL.								
OS	GALLUS GALLUS (CHICKEN).								
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ARCHOSAURIA; AVES;								
OC	NEOGNATHAE; GALLIFORMES; PHASIANIDAE; PHASIANINAE; GALLUS.								
RN	[1]								
RP	SEQUENCE OF 1-50 FROM N.A.								
RX	MEDLINE; 83117850.								
RA	HIRANO H., YAMADA Y., SULLIVAN M., DE CROMBRUGGHE B., PASTAN I.,								
RA	YAMADA K.M.;								
RT	"Isolation of genomic DNA clones spanning the entire fibronectin								
RT	gene.";								
RL	PROC. NATL. ACAD. SCI. U.S.A. 80:46-50(1983).								
RN	[2]								
RP	SEQUENCE OF 51-1256 FROM N.A.								
RC	SPRAIN-WHITE LEHORN;								
RA	NORTON P.A.;								
RL	SUBMITTED (FEB-1995) TO EMBL/GENBANK/DBJ DATA BANKS.								
RN	[3]								
RP	SEQUENCE OF 227-415 FROM N.A.								
RX	MEDLINE; 96183658.								
RA	GERHS A.L., BRANDLI D.W., LEWIS S.D., BENNETT V.D.;								
RT	"The exon encoding the fibronectin type III-9 repeat is								
RT	constitutively included in the mRNA from chick limb mesenchyme and								
RL	cartilage.";								
RL	BIOCHIM. BIOPHYS. ACTA 1311:5-12(1996).								
RN	[4]								
RP	SEQUENCE OF 327-599 FROM N.A.								
RX	MEDLINE; 88050950.								
RA	KUBOMURA S., OBARA M., KARASAKI Y., TANIGUCHI H., GOTOH S.,								
RA	TSUDA T., HIGASHI K., OHSATO K., HIARNO H.;								
RT	"Genetic analysis of the cell binding domain region of the chicken								
RT	fibronectin gene.";								
RL	BIOCHIM. BIOPHYS. ACTA 910:171-181(1987).								
RN	[5]								
RP	SEQUENCE OF 413-1256 FROM N.A.								
RX	MEDLINE; 88142820.								
RA	NORTON P.A., HYNES R.O.;								
RT	"Alternative splicing of chicken fibronectin in embryos and in normal								
RT	and transformed cells.";								
RL	MOL. CELL. BIOL. 7:4297-4307(1987).								

```
Query Match          97.6%; Score 40; DB 1; Length 1256;
Best Local Similarity 83.3%; Pred. NO. 1.94e+00;
Matches             5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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FT DISULFID 1324 1324 INTERCHAIN (WITH 1320 OF OTHER CHAIN) (BY
 FT SITE 461 463 SIMILARITY).
 FT CARBOHYD 89 89 CELL ATTACHMENT SITE.
 SQ SEQUENCE 1328 AA; 145037 MW; 1139F7B6 CRC32;
 Query Match 97.6%; Score 40; DB 1; Length 1328;
 Best Local Similarity 83.3%; Pred. No. 1.94e+00;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Db 460 GRGSP 465
 QY 1 GRGSP 6
 RESULT 3
 ID FINE_BOVIN STANDARD; PRT: 2265 AA.
 AC P07589;
 DT 01-APR-1988 (REL. 07, CREATED)
 DT 01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
 DE FIBRONECTIN (FN).
 GN FN1.
 OS BOS TAURUS (BOVINE).
 OC EUKARYOTA; META20A; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC ARTIODACTYLA; RUMINANTIA; PECORA; BOVIDAE; BOVINAE; BOS.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE; 87054047.
 RA SKORSTENGAARD K., JENSEN M.S., SAHL P., PETERSEN T.E., MAGNUSSON S.;
 RT "Complete primary structure of bovine plasma fibronectin.";
 RL EUR. J. BIOCHEM. 161:441-453(1986).
 RN [2]
 RP PARTIAL SEQUENCE.
 RX MEDLINE; 83117805.
 RA PETERSEN T.E., THORGERSEN H.C., SKORSTENGAARD K., VIBE-PEDERSEN K.,
 RA SAHL P., SOTTRUP-JENSEN L., MAGNUSSON S.;
 RT "Partial primary structure of bovine plasma fibronectin: three types
 of internal homology.";
 RL PROC. NATL. ACAD. SCI. U.S.A. 80:137-141(1983).
 RN [3]
 RP SEQUENCE OF 2170-2265 FROM N.A.
 RX MEDLINE; 83221567.
 RA KORNBILHT A.R., VIBE-PEDERSEN K., BARALLE F.E.;
 RT "Isolation and characterization of cDNA clones for human and bovine
 fibronectins.";
 RL PROC. NATL. ACAD. SCI. U.S.A. 80:3218-3222(1983).
 CC -!- FUNCTION: FIBRONECTINS BIND CELL SURFACES AND VARIOUS COMPOUNDS
 INCLUDING COLLAGEN, FIBRIN, HEPARIN, DNA, AND ACTIN. FIBRONECTINS
 ARE INVOLVED IN CELL ADHESION, CELL MOTILITY, OPSONIZATION, WOUND
 HEALING, AND MAINTENANCE OF CELL SHAPE.
 CC -!- SUBUNIT: MOSTLY HETERODIMERS OR MULTIMERS OF ALTERNATIVELY SPLICED
 VARIANTS, CONNECTED BY 2 DISULFIDE BONDS NEAR THE CARBOXYL ENDS;
 TO A LESSER EXTENT HOMODIMERS.
 CC -!- TISSUE SPECIFICITY: PLASMA FN (SOLUBLE DIMERIC FORM) IS SECRETED
 BY HEPATOCYTES. CELLULAR FN (DIMERIC OR CROSS-LINKED MULTIMERIC
 FORMS), MADE BY FIBROBLASTS, EPITHELIAL AND OTHER CELL TYPES, IS
 DEPOSITED AS FIBRILS IN THE EXTRACELLULAR MATRIX.
 CC -!- ALTERNATIVE PRODUCTS: EACH OF THE "EXTRA DOMAIN" & THE CONNECTING
 STRAND 3 ARE PRESENT IN SOME FORMS OF FIBRONECTIN AND ABSENT IN
 OTHERS. THESE DIFFERENCES ARE DUE TO ALTERNATIVE SPLICING.
 CC -!- SIMILARITY: CONTAINS 12 FIBRONECTIN TYPE I DOMAINS.
 CC -!- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE II DOMAINS.
 CC -!- SIMILARITY: CONTAINS 16 FIBRONECTIN TYPE III DOMAINS.
 CC -----
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 or send an email to license@isb-sib.ch).
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DR EMBL; K00800; E18191; ALT_SEQ.
 DR PIR; A26452; FNBO.
 DR PROSITE; PS00022; EGF_1; 2.
 DR PROSITE; PS00023; FIBRONECTIN_2; 2.
 DR PROSITE; PS01253; FIBRONECTIN_1; 12.
 DR PFAM; PF00039; fn1; 12.
 DR PFAM; PF00040; fn2; 2.
 DR PFAM; PF00041; fn3; 15.
 DR HSSP; P02751; 2FN2.
 KW GLYCOPROTEIN; PLASMA; HEPARIN-BINDING; ACUTE PHASE; PHOSPHORYLATION;
 KW CELL ADHESION; REPEAT; ALTERNATIVE SPLICING.
 FT MOD_RES 1 1
 FT DOMAIN 21 241
 FT DOMAIN 277 577
 FT DNA_BIND 876 1141
 FT DOMAIN 1236 1509
 FT DOMAIN 1600 1870
 FT DOMAIN 1991 2216
 FT DOMAIN 19 59
 FT DOMAIN 64 107
 FT DOMAIN 108 151
 FT DOMAIN 153 197
 FT DOMAIN 198 242
 FT DOMAIN 275 314
 FT DOMAIN 314 373
 FT DOMAIN 374 438
 FT DOMAIN 437 480
 FT DOMAIN 485 527
 FT DOMAIN 528 571
 FT DOMAIN 578 669
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 FT DOMAIN 779 874
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 FT DOMAIN 1055 1141
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 FT DOMAIN 1600 1691
 FT DOMAIN 1892 1780
 FT DOMAIN 1781 1870
 FT DOMAIN 1871 1990
 FT DOMAIN >1870 <1982
 FT DOMAIN 1982 2061
 FT DOMAIN 2061 2127
 FT DOMAIN 2083 2127
 FT DOMAIN 2128 2170
 FT DOMAIN 2172 2215
 FT SITE 1493 1495
 FT DISULFID 21 47
 FT DISULFID 45 56
 FT DISULFID 66 94
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 FT DISULFID 136 148
 FT DISULFID 155 184
 FT DISULFID 182 194
 FT DISULFID 200 229
 FT DISULFID 227 239
 FT DISULFID 277 304
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 FT DISULFID 329 355
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 FT DISULFID 465 477
 FT DISULFID 487 514
 FT DISULFID 512 524
 FT DISULFID 530 558
 FT DISULFID 556 568
 FT DISULFID 2085 2114
 CELL-ATTACHMENT.
 HEPARIN-BINDING 2.
 FIBRIN-BINDING 2.
 FIBRONECTIN TYPE-I 1.
 FIBRONECTIN TYPE-I 2.
 FIBRONECTIN TYPE-I 3.
 FIBRONECTIN TYPE-I 4.
 FIBRONECTIN TYPE-I 5.
 FIBRONECTIN TYPE-I 6.
 FIBRONECTIN TYPE-II 1.
 FIBRONECTIN TYPE-II 2.
 FIBRONECTIN TYPE-I 7.
 FIBRONECTIN TYPE-I 8.
 FIBRONECTIN TYPE-I 9.
 FIBRONECTIN TYPE-III 1.
 FIBRONECTIN TYPE-III 2.
 FIBRONECTIN TYPE-III 3.
 FIBRONECTIN TYPE-III 4.
 FIBRONECTIN TYPE-III 5.
 FIBRONECTIN TYPE-III 6.
 FIBRONECTIN TYPE-III 7.
 FIBRONECTIN TYPE-III 8.
 FIBRONECTIN TYPE-III 9.
 FIBRONECTIN TYPE-III 10.
 FIBRONECTIN TYPE-III 11 (EXTRA DOMAIN).
 FIBRONECTIN TYPE-III 12.
 FIBRONECTIN TYPE-III 13.
 FIBRONECTIN TYPE-III 14.
 CONNECTING STRAND 3 (CS-3) (V REGION).
 FIBRONECTIN TYPE-III 15.
 FIBRONECTIN TYPE-III 16.
 FIBRONECTIN TYPE-I 10.
 FIBRONECTIN TYPE-I 11.
 FIBRONECTIN TYPE-I 12.
 CELL ATTACHMENT SITE.

FT DISULFID 2112 2124
 FT DISULFID 2130 2157
 FT DISULFID 2155 2167
 FT DISULFID 2174 2200
 FT DISULFID 2198 2209
 FT DISULFID 2246 2246
 FT DISULFID 2250 2250
 FT CARBOHYD 399 399
 FT CARBOHYD 497 497
 FT CARBOHYD 511 511
 FT CARBOHYD 846 846
 FT CARBOHYD 976 976
 FT CARBOHYD 1213 1213
 FT CARBOHYD 1967 1967
 FT CARBOHYD 1943 1943
 FT CARBOHYD 1944 1944
 FT MOD_RES 2263 2263
 SQ SEQUENCE 2265 AA; 249557 MW; B5176597 CRC32;

Query Match 97.6%; Score 40; DB 1; Length 2265;
 Best Local Similarity 83.3%; Pred. No. 1.94e+00;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 1492 GRGDSF 1497
 QY 1 GRGESP 6
 |||:|

RESULT 4
 ID FINC_HUMAN STANDARD; PRT: 2386 AA.
 AC P02751; Q14326;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE FIBRONECTIN PRECURSOR (FN).
 GN FN1 OR FN.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
 RN [1]
 RP SEQUENCE OF 1-38 FROM N.A.
 RX GUTMAN A., YAMADA K.M., KORNBLIHT A.;
 RA "Human fibronectin is synthesized as a pre-propolypeptide.";
 RT FEBS LETT. 207:145-148(1986).
 RN [2]
 RP SEQUENCE OF 1-49 FROM N.A.
 RX MEDLINE; 87175578.
 RA DEAN D.C., BOWLUS C.L., BOURGEOIS S.;
 RT "Cloning and analysis of the promoter region of the human fibronectin gene.";
 RL PROC. NATL. ACAD. SCI. U.S.A. 84:1876-1880(1987).
 RN [3]
 RP SEQUENCE OF 32-2081 AND 2113-2386 FROM N.A.
 RX MEDLINE; 85284965.
 RA KORNBLIHT A.R., UMZAWA K., VIBE-PEDERSEN K., BARALLE F.E.;
 RT "Primary structure of human fibronectin: differential splicing may generate at least 10 polypeptides from a single gene.";
 RL EMBO J. 4:1755-1759(1985).
 RN [4]
 RP SEQUENCE OF 973-2081 AND 2113-2386 FROM N.A.
 RX MEDLINE; 84272258.
 RA KORNBLIHT A.R., VIBE-PEDERSEN K., BARALLE F.E.;
 RT "Human fibronectin: cell specific alternative mRNA splicing generates polypeptide chains differing in the number of internal repeats.";
 RL NUCLEIC ACIDS RES. 12:5853-5868(1984).
 RN [5]
 RP SEQUENCE OF 1594-2386 FROM N.A.
 RX MEDLINE; 85280409.
 RA BERNARD M.P., KOLBE M., WEIL D., CHU M.-L.;
 RT "Human cellular fibronectin: comparison of the carboxyl-terminal portion with rat identifies primary structural domains separated by hypervariable regions.";

RL BIOCHEMISTRY 24:2698-2704(1985).
 [6]
 RP SEQUENCE OF 32-290.
 RX MEDLINE; 84032463.
 RA GARCIA-PARDO A., PEARLSTEIN E., FRANGIONE B.;
 RT "Primary structure of human plasma fibronectin. The 29,000-dalton NH2-terminal domain.";
 RL J. BIOL. CHEM. 258:12670-12674(1983).
 [7]
 RP SEQUENCE OF 309-608, AND COLLAGEN-BINDING.
 RX MEDLINE; 87080265.
 RA OWENS R.J., BARALLE F.E.;
 RT "Mapping the collagen-binding site of human fibronectin by expression in *Escherichia coli*.";
 RL EMBO J. 5:2825-2830(1986).
 [8]
 RP SEQUENCE OF 1441-1548.
 RX MEDLINE; 82265604.
 RA PIERSCHBACHER M.D., RUOSLAHTI E., SUNDELIN J., LIND P., PETERSON P.A.;
 RT "The cell attachment domain of fibronectin. Determination of the primary structure.";
 RL J. BIOL. CHEM. 257:9593-9597(1982).
 [9]
 RP SEQUENCE OF 1434-1537 FROM N.A.
 RX MEDLINE; 83290929.
 RA OLDBERG A., LINNEY E., RUOSLAHTI E.;
 RT "Molecular cloning and nucleotide sequence of a cDNA clone coding for the cell attachment domain in human fibronectin.";
 RL J. BIOL. CHEM. 258:10193-10196(1983).
 [10]
 RP SEQUENCE OF 1448-1540 FROM N.A.
 RX MEDLINE; 86111901.
 RA OLDBERG A., RUOSLAHTI E.;
 RT "Evolution of the fibronectin gene. Exon structure of cell attachment domain.";
 RL J. BIOL. CHEM. 261:2113-2116(1986).
 [11]
 RP SEQUENCE OF 1712-1739 FROM N.A.
 RX MEDLINE; 87026578.
 RA SEKIGUCHI K., KLOS A.M., KURACHI K., YOSHITAKE S., HAKOMORI S.;
 RT "Human liver fibronectin complementary DNAs: identification of two different messenger RNAs possibly encoding the alpha and beta subunits of plasma fibronectin.";
 RL BIOCHEMISTRY 25:4936-4941(1986).
 [12]
 RP CHARACTERIZATION OF FIBRIN-BINDING SITE 1.
 RX MEDLINE; 95081153.
 RA ROSTAGNO A., WILLIAMS M.J., BARON M., CAMPBELL I.D., GOLD L.I.;
 RT "Further characterization of the NH2-terminal fibrin-binding site on fibronectin.";
 RL J. BIOL. CHEM. 269:31938-31945(1994).
 [13]
 RP STRUCTURE BY NMR OF 32-92.
 RX MEDLINE; 96069779.
 RA POTTS J.R., PHAN I., WILLIAMS M.J., CAMPBELL I.D.;
 RT "High-resolution structural studies of the factor XIIIa crosslinking site and the first type 1 module of fibronectin.";
 RL NAT. STRUCT. BIOL. 2:946-950(1995).
 [14]
 RP STRUCTURE BY NMR OF 182-275.
 RX MEDLINE; 94141923.
 RA WILLIAMS M.J., PHAN I., HARVEY T.S., ROSTAGNO A., GOLD L.I., CAMPBELL I.D.;
 RT "Solution structure of a pair of fibronectin type 1 modules with fibrin binding activity.";
 RL J. MOL. BIOL. 235:1302-1311(1994).
 [15]
 RP STRUCTURE BY NMR OF 406-464.
 RX MEDLINE; 98179558.
 RA STICHT H., PICKFORD A.R., POTTS J.R., CAMPBELL I.D.;
 RT "Solution structure of the glycosylated second type 2 module of fibronectin.";
 RL J. MOL. BIOL. 276:177-187(1998).

[16] RP STRUCTURE BY NMR OF 1447-1540.
 RX MEDLINE; 93046665.
 RA MAIN A.L., HARVEY T.S., BARON M., BOYD J., CAMPBELL I.D.;
 RT "The three-dimensional structure of the tenth type III module of
 FT fibronectin: an insight into RGD-mediated interactions.";
 RL CELL 71:671-678(1992).
 RN [17]
 RP STRUCTURE BY NMR OF 1447-1540.
 RX MEDLINE; 92162710.
 RA BARON M., MAIN A.L., DRISCOLL P.C., MARDON H.J., BOYD J.,
 RA CAMPBELL I.D.;
 RT "1H NMR assignment and secondary structure of the cell adhesion type
 FT III module of fibronectin.";
 RL BIOCHEMISTRY 31:2068-2073(1992).
 RN [18]
 RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 1447-1535.
 RX MEDLINE; 94166075.
 RA DICKINSON C.D., VEERAPANDIAN B., DAI X.-P., HAMLIN R.C., XUONG N.-H.,
 RA RUOSLAHTI E., ELY K.R.;
 RT "Crystal structure of the tenth type III cell adhesion module of
 FT human fibronectin.";
 RL J. MOL. BIOL. 236:1079-1092(1994).
 CC -!- FUNCTION: FIBRONECTINS BIND CELL SURFACES AND VARIOUS COMPOUNDS
 CC INCLUDING COLLAGEN, FIBRIN, HEPARIN, DNA, AND ACTIN. FIBRONECTINS
 CC ARE INVOLVED IN CELL ADHESION, CELL MOTILITY, OPSONIZATION, WOUND
 CC HEALING, AND MAINTENANCE OF CELL SHAPE.
 CC -!- SUBUNIT: MOSTLY HETERODIMERS OR MULTIMERS OF ALTERNATIVELY SPLICED
 CC VARIANTS, CONNECTED BY 2 DISULFIDE BONDS NEAR THE CARBOXYL ENDS;
 CC TO A LESSER EXTENT HOMODIMERS.
 CC -!- TISSUE SPECIFICITY: PLASMA FN (SOLUBLE DIMERIC FORM) IS SECRETED
 CC BY HEPATOCYTES. CELLULAR FN (DIMERIC OR CROSS-LINKED MULTIMERIC
 CC FORMS), MADE BY FIBROBLASTS, EPITHELIAL AND OTHER CELL TYPES, IS
 CC DEPOSITED AS FIBRILS IN THE EXTRACELLULAR MATRIX.
 CC -!- ALTERNATIVE PRODUCTS: EACH OF THE "EXTRA DOMAIN" & THE CONNECTING
 CC STRAND 3 ARE PRESENT IN SOME FORMS OF FIBRONECTIN AND ABSENT IN
 CC OTHERS. THESE DIFFERENCES ARE DUE TO ALTERNATIVE SPLICING.
 CC -!- SIMILARITY: CONTAINS 12 FIBRONECTIN TYPE I DOMAINS.
 CC -!- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE II DOMAINS.
 CC -!- SIMILARITY: CONTAINS 17 FIBRONECTIN TYPE III DOMAINS.
 CC -----
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 CC -----
 DR EMBL; M15801; G553293; -.
 DR EMBL; X02761; G31397; -.
 DR EMBL; K00055; G182683; -.
 DR EMBL; M10905; G182697; -.
 DR EMBL; M12549; G553294; -.
 DR EMBL; M14059; G182703; -.
 DR PIR; A26460; FNHU.
 DR PDB; ITTF; 31-JAN-94.
 DR PDB; ITTG; 31-JAN-94.
 DR PDB; IFNA; 30-APR-94.
 DR PDB; IFNF; 29-JAN-96.
 DR PDB; IFBR; 15-OCT-95.
 DR PDB; 2FN2; PRELIMINARY.
 DR MIM; I35600; -.
 DR PROSITE; PS00022; EGF_1; 2.
 DR PROSITE; PS00023; FIBRONECTIN_2; 2.
 DR PROSITE; PS01253; FIBRONECTIN_1; 12.
 DR PFAM; PF00039; fn1; 12.
 DR PFAM; PF00040; fn2; 2.
 DR PFAM; PF00041; fn3; 16.
 KW GLYCOPROTEIN; PLASMA; HEPARIN-BINDING; ACUTE PHASE; PHOSPHORYLATION;
 KW SULFATATION; CELL ADHESION; REPEAT; ALTERNATIVE SPLICING; SIGNAL;
 FT 3D-STRUCTURE. 1 31

FT CHAIN 32 2386 FIBRONECTIN.
 FT DOMAIN 52 272 FIBRIN- AND HEPARIN-BINDING 1.
 FT DOMAIN 308 608 COLLAGEN-BINDING.
 FT DNA_BIND 907 1172
 FT DOMAIN 1267 1540 CELL-ATTACHMENT.
 FT DOMAIN 1721 1991 FIBRIN-BINDING 2.
 FT DOMAIN 2206 2337 FIBRIN-BINDING 2.
 FT SITE 1524 1526 CELL ATTACHMENT SITE.
 FT DOMAIN 50 90 FIBRONECTIN TYPE-I 1.
 FT DOMAIN 95 138 FIBRONECTIN TYPE-I 2.
 ...
 Note: remainder of annotations omitted.
 Query Match 97.6%; Score 40; DB 1; Length 2386;
 Best Local Similarity 83.3%; Pred. No. 1.94e+00;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Db 1523 GRGDSF 1528
 Qy 1 GRGESP 6
 |||:|
 1 GRGESP 6
 RESULT 5
 ID FUNC_MOUSE STANDARD; PRT: 2477 AA.
 AC P11276; Q61568; Q61569; Q61567; Q64233;
 DT 01-JUL-1989 (REL. 11, CREATED)
 DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE FIBRONECTIN PRECURSOR (FN) (FRAGMENTS).
 GN FNI.
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.
 RN [1]
 RP SEQUENCE OF 1-28 FROM N.A.
 RC TISSUE-LIVER;
 RX MEDLINE; 94131313.
 RA POLLY P., NICHOLSON R.C.;
 RT "Sequence of the mouse fibronectin-encoding gene promoter region.";
 RL GENE 137:353-354(1993).
 RN [2]
 RP SEQUENCE OF 562-834 FROM N.A.
 RC STRAIN=NMRL;
 RX MEDLINE; 95403556.
 RA TALTS J.F., WELLER A., TIMPL R., EKBLOM M., EKBLOM P.;
 RT "Regulation of mesenchymal extracellular matrix protein synthesis by
 FT transforming growth factor-beta and glucocorticoids in tumor
 FT stroma.";
 RL J. CELL SCI. 108:2153-2162(1995).
 RN [3]
 RP SEQUENCE OF 899-2376 FROM N.A.
 RA GORSKI G., AROS M., NORTON P.;
 RL SUBMITTED (DEC-1995) TO EMBL/GENEBANK/DBBJ DATA BANKS.
 RN [4]
 RP SEQUENCE OF 2375-2477 FROM N.A.
 RX MEDLINE; 88124987.
 RA BLATTI S.P., FOSTER D.N., RANGANATHAN G., MOSES H.L., GETZ M.J.;
 RT "Induction of fibronectin gene transcription and mRNA is a primary
 RT response to growth-factor stimulation of ABR-28 cells.";
 RL PROC. NATL. ACAD. SCI. U.S.A. 85:1119-1123(1988).
 RN [5]
 RP SEQUENCE OF 2375-2477 FROM N.A.
 RC TISSUE-KIDNEY;
 RX MEDLINE; 93011702.
 RA KHANDJIAN E.W., SALOMON C., LEONARD N., TREMBLAY S., TURLER H.;
 RT "Fibronectin gene expression in proliferating, quiescent, and SV40-
 RT infected mouse kidney cells.";
 RL EXP. CELL RES. 202:464-470(1992).
 RN [6]
 RP STRUCTURE BY NMR OF 1447-1630.
 RX MEDLINE; 98202578.
 RA COPIE V., TOMITA-Y., AKIYAMA S.K., AOTA S., YAMADA K.M., VENABLE R.M.,
 RA PASTOR R.W., KRUEGER S., TORCHIA D.A.;

RP SEQUENCE OF 1586-2477 FROM N.A.
 RX MEDLINE; 84082067.
 RA SCHWARZBAUER J.E., TAMKUN J.W., LEWISCHKA I.R., HYNES R.O.;
 RT "Three different fibronectin mRNAs arise by alternative splicing
 within the coding region."
 RL CELL 35;421-431(1983).
 CC !- FUNCTION: FIBRONECTINS BIND CELL SURFACES AND VARIOUS COMPOUNDS
 INCLUDING COLLAGEN, FIBRIN, HEPARIN, DNA, AND ACTIN. FIBRONECTINS
 ARE INVOLVED IN CELL ADHESION, CELL MOTILITY, OPSONIZATION, WOUND
 HEALING, AND MAINTENANCE OF CELL SHAPE.
 CC !- SUBUNIT: MOSTLY HETERODIMERS OR MULTIMERS OF ALTERNATIVELY SPLICED
 VARIANTS, CONNECTED BY 2 DISULFIDE BONDS NEAR THE CARBOXYL ENDS;
 TO A LESSER EXTENT HOMODIMERS.
 CC !- TISSUE SPECIFICITY: PLASMA FN (SOLUBLE DIMERIC FORM) IS SECRETED
 BY HEPATOCYTES. CELLULAR FN (DIMERIC OR CROSS-LINKED MULTIMERIC
 FORMS), MADE BY FIBROBLASTS, EPITHELIAL AND OTHER CELL TYPES, IS
 DEPOSITED AS FIBRILS IN THE EXTRACELLULAR MATRIX.
 CC !- ALTERNATIVE PRODUCTS: EACH OF THE "EXTRA DOMAIN" & THE CONNECTING
 STRAND 3 ARE PRESENT IN SOME FORMS OF FIBRONECTIN AND ABSENT IN
 OTHERS. THESE DIFFERENCES ARE DUE TO ALTERNATIVE SPLICING.
 CC !- SIMILARITY: CONTAINS 12 FIBRONECTIN TYPE I DOMAINS.
 CC !- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE II DOMAINS.
 CC !- SIMILARITY: CONTAINS 18 FIBRONECTIN TYPE III DOMAINS.
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; X15906; G56164; -
 DR EMBL; L29191; G204156; -
 DR EMBL; L00191; G204156; JOINED.
 DR EMBL; L29191; G204157; -
 DR EMBL; L00191; G204157; JOINED.
 DR EMBL; L29191; G204158; -
 DR EMBL; L00191; G204158; JOINED.
 DR EMBL; X05831; G56156; -
 DR EMBL; X05832; G769820; -
 DR EMBL; X05833; G773260; -
 DR EMBL; X05834; G773261; -
 DR PIR; A27252; A27252.
 DR PIR; S00459; S00459.
 DR PIR; S14428; S14428.
 DR PROSITE; PS00022; EGF_1; 2.
 DR PROSITE; PS00023; FIBRONECTIN_2; 2.
 DR PROSITE; PS01253; FIBRONECTIN_1; 12.
 DR PFAM; PF00039; fn1; 12.
 DR PFAM; PF00040; fn2; 2.
 DR PFAM; PF00041; fn3; 17.
 DR HSP; P02751; 1FBR.
 KW GLYCOPROTEIN; PLASMA; HEPARIN-BINDING; ACUTE PHASE; PHOSPHORYLATION;
 KW SULFATATION; CELL ADHESION; REPEAT; ALTERNATIVE SPLICING; SIGNAL.
 FT SIGNAL 1 32
 FT CHAIN 33 2477 FIBRONECTIN.
 FT DOMAIN 53 273 FIBRIN- AND HEPARIN-BINDING 1.
 FT DOMAIN 308 608 COLLAGEN-BINDING.
 FT DNA_BIND 906 1171
 FT DOMAIN 1337 1630 CELL-ATTACHMENT.
 FT DOMAIN 1811 2081 HEPARIN-BINDING 2.
 FT DOMAIN 2296 2427 FIBRIN-BINDING 2.
 FT DOMAIN 51 91 FIBRONECTIN TYPE-I 1.
 FT DOMAIN 96 139 FIBRONECTIN TYPE-I 2.
 FT DOMAIN 140 183 FIBRONECTIN TYPE-I 3.
 FT DOMAIN 185 229 FIBRONECTIN TYPE-I 4.
 FT DOMAIN 230 274 FIBRONECTIN TYPE-I 5.
 FT DOMAIN 306 345 FIBRONECTIN TYPE-I 6.
 FT DOMAIN 345 404 FIBRONECTIN TYPE-II 1.
 FT DOMAIN 405 469 FIBRONECTIN TYPE-II 2.
 FT DOMAIN 468 511 FIBRONECTIN TYPE-I 7.
 FT DOMAIN 516 558 FIBRONECTIN TYPE-I 8.

Query Match

Score 40; DB 1; Length 2477;

Best Local Similarity 83.3%;

Pred. No. 1.94e+00;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

MW; 093A8F76 CRC32;

97.68;

Score 40; DB 1; Length 2477;

Pred. No. 1.94e+00;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

MW; 093A8F76 CRC32;

Query Match

Score 40; DB 1; Length 2477;

Best Local Similarity 83.3%;

Pred. No. 1.94e+00;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

MW; 093A8F76 CRC32;

97.68;

Score 40; DB 1; Length 2477;

Pred. No. 1.94e+00;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

MW; 093A8F76 CRC32;

Query Match

Score 40; DB 1; Length 2477;

Best Local Similarity 83.3%;

Pred. No. 1.94e+00;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

MW; 093A8F76 CRC32;

97.68;

Score 40; DB 1; Length 2477;

Pred. No. 1.94e+00;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

MW; 093A8F76 CRC32;

Query Match

Score 40; DB 1; Length 2477;

Best Local Similarity 83.3%;

Pred. No. 1.94e+00;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

MW; 093A8F76 CRC32;

97.68;

Score 40; DB 1; Length 2477;

Pred. No. 1.94e+00;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

MW; 093A8F76 CRC32;

Query Match

Score 40; DB 1; Length 2477;

Best Local Similarity 83.3%;

Pred. No. 1.94e+00;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

MW; 093A8F76 CRC32;

97.68;

Score 40; DB 1; Length 2477;

Pred. No. 1.94e+00;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

MW; 093A8F76 CRC32;

Query Match

Score 40; DB 1; Length 2477;

Best Local Similarity 83.3%;

Pred. No. 1.94e+00;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

MW; 093A8F76 CRC32;

97.68;

Score 40; DB 1; Length 2477;

Pred. No. 1.94e+00;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

MW; 093A8F76 CRC32;

Query Match

Score 40; DB 1; Length 2477;

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Pred. No. 1.94e+00;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

MW; 093A8F76 CRC32;

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Score 40; DB 1; Length 2477;

Pred. No. 1.94e+00;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Query Match

Score 40; DB 1; Length 2477;

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Pred. No. 1.94e+00;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

MW; 093A8F76 CRC32;

97.68;

Score 40; DB 1; Length 2477;

Pred. No. 1.94e+00;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

MW; 093A8F76 CRC32;

Query Match

Score 40; DB 1; Length 2477;

Best Local Similarity 83.3%;

Pred. No. 1.94e+00;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

MW; 093A8F76 CRC32;

97.68;

Score 40; DB 1; Length 2477;

Pred. No. 1.94e+00;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

MW; 093A8F76 CRC32;

Query Match

Score 40; DB 1; Length 2477;

Best Local Similarity 83.3%;

Pred. No. 1.94e+00;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

MW; 093A8F76 CRC32;

97.68;

Score 40; DB 1; Length 2477;

Pred. No. 1.94e+00;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

MW; 093A8F76 CRC32;

Query Match

Score 40; DB 1; Length 2477;

Best Local Similarity 83.3%;

Pred. No. 1.94e+00;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

MW; 093A8F76 CRC32;

97.68;

Score 40; DB 1; Length 2477;

Pred. No. 1.94e+00;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

MW; 093A8F76 CRC32;

Query Match

Score 40; DB 1; Length 2477;

Best Local Similarity 83.3%;

Pred. No. 1.94e+00;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

MW; 093A8F76 CRC32;

97.68;

Score 40; DB 1; Length 2477;

Pred. No. 1.94e+00;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

MW; 093A8F76 CRC32;

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Score 40; DB 1; Length 2477;

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MW; 093A8F76 CRC32;

97.68;

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Pred. No. 1.94e+00;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

MW; 093A8F76 CRC32;

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Score 40; DB 1; Length 2477;

Best Local Similarity 83.3%;

Pred. No. 1.94e+00;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

MW; 093A8F76 CRC32;

97.68;

Score 40; DB 1; Length 2477;

Pred. No. 1.94e+00;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

MW; 093A8F76 CRC32;

Query Match

Score 40; DB 1; Length 2477;

Best Local Similarity 83.3%;

Pred. No. 1.94e+00;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

MW; 093A8F76 CRC32;

97.68;

Score 40; DB 1; Length 2477;

Pred. No. 1.94e+00;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

MW; 093A8F76 CRC32;

Query Match

Score 40; DB 1; Length 2477;

Best Local Similarity 83.3%;

Pred. No. 1.94e+00;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

MW; 093A8F76 CRC32;

97.68;

Score 40; DB 1; Length 2477;

Pred. No. 1.94e+00;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

MW; 093A8F76 CRC32;

Query Match

Score 40; DB 1; Length 2477;

Best Local Similarity 83.3%;

Pred. No. 1.94e+00;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

MW; 093A8F76 CRC32;

97.68;

Score 40; DB 1; Length 2477;

Pred. No. 1.94e+00;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

MW; 093A8F76 CRC32;

Query Match

Score 40; DB 1; Length 2477;

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Pred. No. 1.94e+00;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

MW; 093A8F76 CRC32;

97.68;

Score 40; DB 1; Length 2477;

Pred. No. 1.94e+00;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

MW; 093A8F76 CRC32;

Query Match

Score 40; DB 1; Length 2477;

Best Local Similarity 83.3%;

Pred. No. 1.94e+00;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

MW; 093A8F76 CRC32;

97.68;

Score 40; DB 1; Length 2477;

Pred. No. 1.94e+00;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

MW; 093A8F76 CRC32;

Query Match

Score 40; DB 1; Length 2477;

Best Local Similarity 83.3%;

Pred. No. 1.94e+00;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

MW; 093A8F76 CRC32;

97.68;

Score 40; DB 1; Length 2477;

Pred. No. 1.94e+00;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

MW; 093A8F76 CRC32;

Query Match

Score 40; DB 1; Length 2477;

Best Local Similarity 83.3%;

Pred. No. 1.94e+00;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

MW; 093A8F76 CRC32;

97.68;

Score 40; DB 1; Length 2477;

Pred. No. 1.94e+00;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

MW; 093A8F76 CRC32;

Query Match

Score 40; DB 1; Length 2477;

Best Local Similarity 83.3%;

Pred. No. 1.94e+00;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

MW; 093A8F76 CRC32;

97.68;

Score 40; DB 1; Length 2477;

Pred. No. 1.94e+00;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

MW; 093A8F76 CRC32;

Query Match

Score

```

Db 1613 GRGDSP 1618
QY 1 GRGSP 6

RESULT 7
ID FINC_XENLA STANDARD; PRT; 2481 AA.
AC Q91740;
DT 01-NOV-1997 (REL. 35, CREATED)
DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE FIBRONECTIN PRECURSOR.
GN FNI.

OS XENOPUS LAEVIS (AFRICAN CLAWED FROG).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; AMPHIBIA; BATRACHIA; ANURA;
OC MESOBATRACHIA; PIPOIDEA; PIPIDAE; XENOPODINAE; XENOPUS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 92111942.
RA DESIMONE D.W., NORTON P.A., HYNES R.O.;
RT "Identification and characterization of alternatively spliced
  fibronectin mRNAs expressed in early Xenopus embryos.";
RL DEV. BIOL. 149:357-369(1992).
CC -!- FUNCTION: FIBRONECTINS BIND CELL SURFACES AND VARIOUS COMPOUNDS
  INCLUDING COLLAGEN, FIBRIN, HEPARIN, DNA, AND ACTIN. FIBRONECTINS
  ARE INVOLVED IN CELL ADHESION, CELL MOTILITY, OPSONIZATION, WOUND
  HEALING, AND MAINTENANCE OF CELL SHAPE (BY SIMILARITY).
CC -!- SUBUNIT: DIMERS OR MULTIMERS OF ALTERNATIVELY SPLICED VARIANTS,
  CONNECTED BY 2 DISULFIDE BONDS NEAR THE CARBOXYL ENDS (BY
  SIMILARITY).
CC -!- TISSUE SPECIFICITY: IN EARLY XENOPUS EMBRYO, CELLULAR FORMS OF
  FIBRONECTIN PREDOMINATE WHICH INCLUDE BOTH EXTRA DOMAINS. IN
  FIBRONECTIN OF EMBRYONIC AND ADULT LIVER THE CONNECTING STRAND 3
  CAN BE EITHER COMPLETELY EXCLUDED OR INCLUDED.
CC -!- ALTERNATIVE PRODUCTS: EACH OF THE "EXTRA DOMAIN" & THE CONNECTING
  STRAND 3 ARE PRESENT IN SOME FORMS OF FIBRONECTIN AND ABSENT IN
  OTHERS. THESE DIFFERENCES ARE DUE TO ALTERNATIVE SPLICING.
CC -!- SIMILARITY: CONTAINS 12 FIBRONECTIN TYPE I DOMAINS.
CC -!- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE II DOMAINS.
CC -!- SIMILARITY: CONTAINS 18 FIBRONECTIN TYPE III DOMAINS.
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or send an email to license@isb-sib.ch).
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DR EMBL; M77820; G214134; -.
DR PROSITE; PS00022; EGF_1; 2.
DR PROSITE; PS01253; FIBRONECTIN_1; 11.
DR PFAM; PF00039; fn1; 12.
DR PFAM; PF00040; fn2; 2.
DR PFAM; PF00041; fn3; 17.
DR HSSP; P02751; 2FN2.
KW GLYCOPROTEIN; PLASMA; HEPARIN-BINDING; ACUTE PHASE; CELL ADHESION;
KW REPEAT; ALTERNATIVE SPLICING; SIGNAL.
FT SIGNAL 1 31
FT CHAIN 32 2481
FT DOMAIN 55 275 FIBRONECTIN.
FT DOMAIN 309 609 FIBRIN- AND HEPARIN-BINDING 1.
FT DNA_BIND 907 1172 COLLAGEN-BINDING.
FT DOMAIN 1358 1631 BY SIMILARITY.
FT DOMAIN 1812 2082 CELL-ATTACHMENT.
FT DOMAIN 2301 2432 HEPARIN-BINDING 2.
FT DOMAIN 53 93 FIBRONECTIN TYPE-1.
FT DOMAIN 98 141 FIBRONECTIN TYPE-I 2.
FT DOMAIN 142 185 FIBRONECTIN TYPE-I 3.
FT DOMAIN 187 231 FIBRONECTIN TYPE-I 4.
FT DOMAIN 232 276 FIBRONECTIN TYPE-I 5.
FT DOMAIN 307 346 FIBRONECTIN TYPE-I 6.

FT DOMAIN 346 405 FIBRONECTIN TYPE-II 1.
FT DOMAIN 406 470 FIBRONECTIN TYPE-II 2.
FT DOMAIN 469 512 FIBRONECTIN TYPE-I 7.
FT DOMAIN 517 559 FIBRONECTIN TYPE-I 8.
FT DOMAIN 560 603 FIBRONECTIN TYPE-I 9.
FT DOMAIN 610 707 FIBRONECTIN TYPE-III 1.
FT DOMAIN 708 809 FIBRONECTIN TYPE-III 2.
FT DOMAIN 810 904 FIBRONECTIN TYPE-III 3.
FT DOMAIN 905 995 FIBRONECTIN TYPE-III 4.
FT DOMAIN 1086 1173 FIBRONECTIN TYPE-III 5.
FT DOMAIN 1174 1265 FIBRONECTIN TYPE-III 6.
FT DOMAIN 1266 1356 FIBRONECTIN TYPE-III 7.
FT DOMAIN 1357 1447 FIBRONECTIN TYPE-III 8 (EXTRA DOMAIN).
FT DOMAIN 1448 1537 FIBRONECTIN TYPE-III 9.
FT DOMAIN 1538 1631 FIBRONECTIN TYPE-III 10.
FT DOMAIN 1632 1721 FIBRONECTIN TYPE-III 11.
FT DOMAIN 1722 1811 FIBRONECTIN TYPE-III 12.
FT DOMAIN 1812 1903 FIBRONECTIN TYPE-III 13 (EXTRA DOMAIN).
FT DOMAIN 1904 1992 FIBRONECTIN TYPE-III 14.
FT DOMAIN 1993 2082 FIBRONECTIN TYPE-III 15.
FT DOMAIN 2083 2205 CONNECTING STRAND 3 (CS-3) (V REGION).
FT DOMAIN >2082 <2206 FIBRONECTIN TYPE-III 17.
FT DOMAIN 2206 2287 FIBRONECTIN TYPE-III 18.
FT DOMAIN 2289 2343 FIBRONECTIN TYPE-I 10.
FT DOMAIN 2344 2386 FIBRONECTIN TYPE-I 11.
FT DOMAIN 2388 2431 FIBRONECTIN TYPE-I 12.
FT SITE 1615 1617 CELL ATTACHMENT SITE.
FT DISULFID 55 81 BY SIMILARITY.
FT DISULFID 79 90 BY SIMILARITY.
FT DISULFID 100 128 BY SIMILARITY.
FT DISULFID 126 138 BY SIMILARITY.
FT DISULFID 144 172 BY SIMILARITY.
FT DISULFID 170 182 BY SIMILARITY.
FT DISULFID 189 218 BY SIMILARITY.
FT DISULFID 216 228 BY SIMILARITY.
FT DISULFID 234 263 BY SIMILARITY.
FT DISULFID 261 273 BY SIMILARITY.
FT DISULFID 309 336 BY SIMILARITY.
FT DISULFID 334 343 BY SIMILARITY.
FT DISULFID 361 387 BY SIMILARITY.
FT DISULFID 375 402 BY SIMILARITY.
FT DISULFID 421 447 BY SIMILARITY.
FT DISULFID 471 499 BY SIMILARITY.
FT DISULFID 497 509 BY SIMILARITY.
FT DISULFID 519 546 BY SIMILARITY.
FT DISULFID 544 556 BY SIMILARITY.
FT DISULFID 562 590 BY SIMILARITY.
FT DISULFID 588 600 BY SIMILARITY.
FT DISULFID 2301 2330 BY SIMILARITY.
FT DISULFID 2328 2340 BY SIMILARITY.
FT DISULFID 2346 2373 BY SIMILARITY.
FT DISULFID 2371 2383 BY SIMILARITY.
FT DISULFID 2390 2414 BY SIMILARITY.
FT DISULFID 2412 2428 BY SIMILARITY.
FT DISULFID 2429 2459 INTERCHAIN (WITH 2463 OF OTHER CHAIN) (BY
  SIMILARITY).
FT DISULFID 2463 2463 INTERCHAIN (WITH 2459 OF OTHER CHAIN) (BY
  SIMILARITY).
FT CARBOHYD 431 431 POTENTIAL.
FT CARBOHYD 529 529 POTENTIAL.
FT CARBOHYD 543 543 POTENTIAL.
FT CARBOHYD 877 877 POTENTIAL.
FT CARBOHYD 1244 1244 POTENTIAL.
FT CARBOHYD 1291 1291 POTENTIAL.
FT CARBOHYD 2202 2202 POTENTIAL.
SQ SEQUENCE 2481 AA; 272678 MW; 1C0F3341 CRC32;

Query Match 97.6%; Score 40; DB 1; Length 2481;
Best Local Similarity 83.3%; Pred. No. 1.94e+00;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Db 1614 GRGDSP 1619

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QY      1 GRGESP 6
      111111
RESULT      8
ID      YIK3-YEAST      STANDARD;      PRT;      425 AA.
AC      P04087;
DT      01-FEB-1995 (REL. 31, CREATED)
DT      01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
DT      01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE      HYPOTHETICAL 48.3 KD PROTEIN IN MOB1-SGA1 INTERGENIC REGION.
GN      YIL103W.
OS      SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
OC      EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOMYCETES; SACCHAROMYCETALES;
OC      SACCHAROMYCETACEAE; SACCHAROMYCES.
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=S288C / AB972;
RA      BARRELL B.G., BADCOCK K., BANKIER A.T., BOWMAN S., BROWN D.,
RA      CHURCHER C.M., CONNOR R., CORSEY T., DEAR S., DEVLIN K., FRASER A.,
RA      GENTLES S., HAMLYN N., HORSNELL T.S., HUNT S., JAGELS K., JONES M.,
RA      LOUIS E., LYE G., MOULE T., MOULE T., ODELL C., PEARSON D.,
RA      RAJANDREAM M.A., RILES L., ROWLEY N., SKELTON J., SMITH V.,
RA      WALSH S.V., WHITEHEAD S.;
RL      SUBMITTED (DEC-1994) TO EMBL/GENBANK/DBJ DATA BANKS.
CC      -1- SIMILARITY: TO YEAST DIPHTHERIA TOXIN RESISTANCE PROTEIN 2 (DPH2),
CC      TO S.POMBE SPAC13F4.15C, TO C.ELEGANS C09G5.2, C14B1.5 AND
CC      M.JANNASCHII MJ0483.
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CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
-----
CC      EMBL; Z38125; G558703;
CC      EMBL; Z47047; G763243;
CC      PIR; S48469; S48469.
CC      HYPOTHETICAL PROTEIN.
QY      SEQUENCE 425 AA; 48310 MW; 28921DCE CRC32;

Query Match      95.1%; Score 39; DB 1; Length 425;
Best Local Similarity 83.3%; Pred. No. 3.67e+00;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db      415 GRGETP 420
      111111
QY      1 GRGESP 6
      111111
RESULT      9
ID      Y863-SYNY3      STANDARD;      PRT;      463 AA.
AC      P73754;
DT      15-JUL-1998 (REL. 36, CREATED)
DT      15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
DT      15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE      HYPOTHETICAL 50.4 KD PROTEIN SLR0863.
GN      SLR0863.
OS      SYNECHOCYSTIS SP. (STRAIN PCC 6803).
OC      BACTERIA; CYANOBACTERIA; CHROCOCCALES; SYNECHOCYSTIS.
RN      [1]
RP      SEQUENCE FROM N.A.
RC      MEDLINE; 97061201.
RA      KANEKO T., SATO S., KOTANI H., TANAKA A., ASAMIZU E., NAKAMURA Y.,
RA      MIYAJIMA N., HIROSAWA M., SUGIURA M., SASAMOTO S., KIMURA T.,
RA      HOSOUCHI T., MURAKAMI A., MURAKAMI A., NAKAZAKI N., NARUO K.,
RA      OKUMURA S., SHIMPO S., TAKEUCHI C., WADA T., WATANABE A.,
RA      YAMADA M., YASUDA M., TABATA S.;
RT      "Sequence analysis of the genome of the unicellular cyanobacterium
RT      Synechocystis sp. Strain PCC6803. II. Sequence determination of the
RT      entire genome and assignment of potential protein-coding regions.";
-----
CC      DNA RES. 3:109-136(1996).
CC      -1- SIMILARITY: BELONGS TO THE TLDD/PMBA FAMILY.
-----
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-----
CC      EMBL; D90909; G1652888;
CC      HYPOTHETICAL PROTEIN.
QY      SEQUENCE 463 AA; 50369 MW; FE40976C CRC32;

Query Match      95.1%; Score 39; DB 1; Length 463;
Best Local Similarity 83.3%; Pred. No. 3.67e+00;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db      352 GRGETP 357
      111111
QY      1 GRGESP 6
      111111
RESULT      10
ID      FILA_MOUSE      STANDARD;      PRT;      336 AA.
AC      P11088;
DT      01-JUL-1989 (REL. 11, CREATED)
DT      01-JUL-1989 (REL. 11, LAST SEQUENCE UPDATE)
DT      01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE      FILAGGRIN (FRAGMENT).
GN      FLG.
OS      MUS MUSCULUS (MOUSE).
OC      EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC      RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.
RN      [1]
RP      SEQUENCE FROM N.A.
RC      MEDLINE; 88058903.
RA      ROTHNAGEL J.A., MEHREL T., IDLER W.W., ROOP D.R., STEINERT P.M.;
RT      "The gene for mouse epidermal filaggrin precursor. Its partial
RT      characterization, expression, and sequence of a repeating filaggrin
RT      unit.";
RL      J. BIOL. CHEM. 262:15643-15648(1987).
RN      [2]
RP      REVISIONS.
RA      ROTHNAGEL J.A.;
RL      SUBMITTED (SEP-1988) TO EMBL/GENBANK/DBJ DATA BANKS.
CC      -1- FUNCTION: FILAGGRIN AGGREGATES KERATIN INTERMEDIATE FILAMENTS
CC      AND PROMOTES DISULFID-BOND FORMATION AMONGST THE INTERMEDIATE
CC      FILAMENTS DURING TERMINAL DIFFERENTIATION OF MAMMALIAN
CC      EPIDERMIS.
CC      -1- PTM: FILAGGRIN IS INITIALLY SYNTHESIZED AS A LARGE, INSOLUBLE,
CC      HIGHLY PHOSPHORYLATED PRECURSOR CONTAINING MANY TANDEM COPIES
CC      OF 248 AA, WHICH ARE NOT SEPARATED BY "LARGE LINKER". THE
CC      PRECURSOR IS DEPOSITED AS KERATOHYALIN GRANULES. DURING TERMINAL
CC      DIFFERENTIATION IT IS DEPHOSPHORYLATED & PROTEOLYTICALLY CLEAVED.
-----
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-----
CC      EMBL; J03458; G387157;
CC      PIR; A28444; A28444.
CC      MGD; MGI:95553; FLG.
CC      PHOSPHORYLATION; POLYPROTEIN; DEVELOPMENTAL PROTEIN.
CC      NON_TER 1
QY      SEQUENCE 336 AA; 35678 MW; 44E31E65 CRC32;

Query Match      92.7%; Score 38; DB 1; Length 336;

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CC -!- CATALYTIC ACTIVITY: A STEROID + AH(2) + O(2) - A 21-HYDROXYSTEROID
CC + A + H(2)O.
CC -!- SUBCELLULAR LOCATION: MEMBRANE-BOUND. ENDOPLASMIC RETICULUM.
CC -!- DOMAIN: THE LEUCINE-RICH HYDROPHOBIC AMINO ACID N-TERMINAL REGION
CC PROBABLY HELPS TO ANCHOR THE PROTEIN TO THE MICROSMAL MEMBRANE.
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
CC PIR: A32525; A32525
CC DR PROSITE; PS00086; CYTOCHROME_P450; 1.
CC DR PFAM; PF00067; P450; 1.
CC KW OXIDOREDUCTASE; MONOOXYGENASE; MEMBRANE; HEME; MICROsome;
CC ENDOPLASMIC RETICULUM; STEROIDGENESIS; STEROID-BINDING.
CC FT BINDING 427 427
CC FT DOMAIN 341 357
CC SQ SEQUENCE 492 AA; 55518 MW; 9A721CE0 CRC32;

Query Match 92.7%; Score 38; DB 1; Length 492;
Best Local Similarity 83.3%; Pred. No. 6.87e+00;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 484 GRGESP 489
QY 1 GRGESP 6

RESULT 14
ID CPEL_BOVIN STANDARD; PRT; 495 AA.
AC O18963;
DT 15-DEC-1998 (REL. 37, CREATED)
DT 15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE)
DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
DE CYTOCHROME P450 2EL (EC 1.14.14.1) (CYP11E1).
GN CYP2E1.
OS BOS TAURUS (BOVINE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC ARTIODACTYLA; RUMINANTIA; PECORA; BOVIDAE; BOVINAE; BOS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HEREFORD; TISSUE=LIVER;
RA VAN RAAK M., NATSUHORI M., LICHTENBERG M., KLEIJ L., TEN BERGHE D.,
RA DE GROENE E.M., VAN MIERT A.S., WITKAMP R.F., HORBACH G.J.;
RT "Isolation of a full length cytochrome P450 (CYP2E) cDNA sequence and
RT its functional expression in v79 cells.";
RL SUBMITTED (OCT-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -!- FUNCTION: CYTOCHROMES P450 ARE A GROUP OF HEME-THIOLATE
CC MONOOXYGENASES. IN LIVER MICROSOMES, THIS ENZYME IS INVOLVED IN AN
CC NADPH-DEPENDENT ELECTRON TRANSPORT PATHWAY. IT OXIDIZES A VARIETY
CC OF STRUCTURALLY UNRELATED COMPOUNDS, INCLUDING STEROIDS, FATTY
CC ACIDS, AND XENOBIOTICS.
CC -!- CATALYTIC ACTIVITY: RH + REDUCED FLAVOPROTEIN + O(2) - ROH +
CC OXIDIZED FLAVOPROTEIN + H(2)O.
CC -!- SUBCELLULAR LOCATION: MEMBRANE-BOUND. ENDOPLASMIC RETICULUM.
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
CC
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CC
CC EMBL; AJ001715; E354269; -
CC DR PROSITE; PS00086; CYTOCHROME_P450; 1.
CC DR PFAM; PF00067; P450; 1.
CC KW OXIDOREDUCTASE; MONOOXYGENASE; ELECTRON TRANSPORT; MEMBRANE; HEME;
CC MICROsome; ENDOPLASMIC RETICULUM.
CC FT BINDING 437 437
CC SQ SEQUENCE 495 AA; 56827 MW; 3F2B6FCE CRC32;

Query Match 92.7%; Score 38; DB 1; Length 495;
Best Local Similarity 83.3%; Pred. No. 6.87e+00;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Db 99 GRGESP 104
QY 1 GRGESP 6

RESULT 15
ID YNM7_YEAST STANDARD; PRT; 953 AA.
AC P53917;
DT 01-OCT-1996 (REL. 34, CREATED)
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE HYPOTHETICAL 109.8 KD PROTEIN IN CPT1-SFC98 INTERGENIC REGION.
GN YNL127W OR N1221 OR N1875.
OS SACHAROMYCES CEREVISIAE (BAKER'S YEAST).
OC EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOMYCETES; SACHAROMYCETALES;
OC SACHAROMYCETACEAE; SACHAROMYCES.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RX MEDLINE; 96109932.
RA MALLET L., BUSSEAU F., JACQUET M.;
RT "A 43.5 kb segment of yeast chromosome XIV, which contains MFA2,
RT MEP2, CAP/SRV2, NAM9, FKBI/FPB1/RBP1, MOM22 and CPT1, predicts an
RT adenosine deaminase gene and 14 new open reading frames.";
RL YEAST 11:1195-1209(1995).
RN [2]
RP SEQUENCE OF 26-953 FROM N.A.
RX MEDLINE; 97245296.
RA DE ANTONI A., D'ANGELO M., DAL PERO F., SARTORELLO F., PANDOLFO D.,
RA PALLAVICINI A., LANFRANCHI G., VALLE G.;
RT "The DNA sequence of cosmid 14-13b from chromosome XIV of
RT Saccharomyces cerevisiae reveals an unusually high number of
RT overlapping open reading frames.";
RL YEAST 13:261-266(1997).
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CC
CC EMBL; Z46843; G510324; -
CC DR EMBL; Z71402; E328838; -
CC DR EMBL; Z71403; E239941; -
CC DR EMBL; Z69382; E221820; -
CC DR HSSP; P03036; 3CRO.
KW HYPOTHETICAL PROTEIN.
SQ SEQUENCE 953 AA; 103792 MW; B20E49F6 CRC32;

Query Match 92.7%; Score 38; DB 1; Length 953;
Best Local Similarity 83.3%; Pred. No. 6.87e+00;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 369 GRGESP 374
QY 1 GRGESP 6

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